

OIPE

J Murphy

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/445,258

DATE: 07/16/2001
TIME: 11:37:50

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\07162001\I445258.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Kato, Seishi
5 Sekine, Shingo
6 Kimura, Tomoko
8 <120> TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
9 DOMAINS AND DNAS ENCODING THESE PROTEINS
13 <130> FILE REFERENCE: GIN-6706CPUS
15 <140> CURRENT APPLICATION NUMBER: 09/445,258
16 <141> CURRENT FILING DATE: 1999-12-01
18 <150> PRIOR APPLICATION NUMBER: PCT/US98/02445
19 <151> PRIOR FILING DATE: 1998-06-03
21 <150> PRIOR APPLICATION NUMBER: JP 9-144948
22 <151> PRIOR FILING DATE: 1997-06-03
24 <160> NUMBER OF SEQ ID NOS: 54
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

2501 <210> SEQ ID NO: 54			
2502 <211> LENGTH: 1914			
2503 <212> TYPE: DNA			
2504 <213> ORGANISM: Homo sapiens			
2506 <220> FEATURE:			
2507 <221> NAME/KEY: CDS			
2508 <222> LOCATION: (80)...(661)			
2510 <400> SEQUENCE: 54			
2511 actctctgtct gtcgcccgtc ccgcgcgtc ctccgaccccg ctccgctccg ctccgctcgg	60		
2512 ccccgcccg cccgtcaac atg atc cgc tgc ggc ctg gcc tgc gag cgc tgc	112		
Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys			
2514 1 5 10			
2516 cgc tgg atc ctg ccc ctg ctc cta ctc agc gcc atc gcc ttc gac atc	160		
2517 Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile			
2518 15 20 25			
2520 atc gcg ctg gcc ggc cgc ggc tgg ttg cag tct agc gac cac ggc cag	208		
2521 Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln			
2522 30 35 40			
2524 acg tcc tcg ctg tgg tgg aaa tgc tcc caa gag ggc ggc ggc agc ggg	256		
2525 Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Ser Gly			
2526 45 50 55			
2528 tcc tac gag gag ggc tgt cag agc ctc atg gag tac gcg tgg ggt aga	304		
2529 Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg			
2530 60 65 70 75			
2532 gca gcg gct gcc atg ctc ttc tgt ggc ttc atc atc ctg gtg atc tgt	352		
2533 Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys			
2534 80 85 90			
2536 ttc atc ctc tcc ttc ttc gcc ctc tgt gga ccc cag atg ctt gtc ttc	400		
2537 Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe			

RAW SEQUENCE LISTING
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2538	95	100	105	
2540	ctg aga gtg att gga ggt ctc ctt gcc ttg gct gct gtg ttc cag atc			448
2541	Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile			
2542	110	115	120	
2544	atc tcc ctg gta att tac ccc gtg aag tac acc cag acc ttc acc ctt			496
2545	Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu			
2546	125	130	135	
2548	cat gcc aac cgt gct gtc act tac atc tat aac tgg gcc tac ggc ttt			544
2549	His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe			
2550	140	145	150	155
2552	ggg tgg gca gcc acg att atc ctg atc ggc tgt gcc ttc ttc ttc tgc			592
2553	Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys			
2554	160	165	170	
2556	tgc ctc ccc aac tac gaa gat gac ctt ctg ggc aat gcc aag ccc agg			640
2557	Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg			
2558	175	180	185	
2560	tac ttc tac aca tct gcc taa ctggaaatg aatgtggag aaaatcgctg			691
2561	Tyr Phe Tyr Thr Ser Ala *			
2562	190			
2564	ctgctgagat ggactccaga agaagaaact gtttctccag gcgactttga acccattttt			751
2565	tggcagtgtt catattatta aactagtcaa ataagctaaa ataatttggg agaaaaatatt			811
2566	tttaaagttag tgttatagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt			871
2567	ttcactaatt acctatacta tgccaatatt tccttatatc tatccataac atttatacta			931
2568	catttgttaag agaatatgca cgtgaaactt aacactttat aaggtaaaaa tgaggttcc			991
2569	aagatthaat aatctgatca agttcttgat atttccaaat agaatggact tggctgttta			1051
2570	agggctaagg agaagaggaa gataaggta aaagttgtta atgacccaaac attctaaaag			1111
2571	aaatgcaaaa aaaaagttt tttcaagcc ttcaactat ttaaggaaag caaaatcatt			1171
2572	tcctaaatgc atatcatttg tgagaatttc tcattaatat cctgaatcat tcatttcagc			1231
2573	taaggcttca tggtgactcg atatgtcatc taggaaagta ctatccatg gtccaaacct			1291
2574	gttgcctatag ttggtaaggc ttcccttaa gtgtgaaata ttttagatgaa attttctt			1351
2575	ttaaagtctt ttatagggtt agggtgtgg aaaatgctat attaataat ctgttagtgtt			1411
2576	ttgtgtttat atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt			1471
2577	atcatgactg atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattctgtc			1531
2578	acaaaagtgc cactaaaaca gcctcaggag aataaatgac ttgctttct aaatctcagg			1591
2579	tttatctggg ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc			1651
2580	tacatatagt taaaatcctg gtctttctt gtaaaacagat tttaaatgtc tgatataaaa			1711
2581	catgccacag gagaattcgg ggatttgagt ttctctgaat agcatatata tgatgcatcg			1771
2582	gataggtcat tatgatttt taccatttcg actcacataa tgaaaaccaa ttcattttaa			1831
2583	atatcagatt attatgtt aagttgtgaa aaaagctaat tgttagtttc attatgaagt			1891
2584	tttcccaata aaccaggat tct			1914

E--> 2585 *gin-6706cPus 9* *delete*

VERIFICATION SUMMARY

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L:2585 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:54
L:2585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2585 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:1922 SEQ:54
L:2585 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:2585 M:112 C: (48) String data converted to lower case,
L:2585 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1914 Found:1922 SEQ:54